Amendments to the Specification:

Please replace the paragraph beginning at page 12, line 6, with the following rewritten paragraph:

Another example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and the BLAST 2.0 algorithm, which are described in Altschul *et al., J. Mol. Biol.* 215:403-410 (1990) and Altschul *et al., Nucleic Acids Res.* 25:3389-3402 (1977)). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~. The BLASTN program (for nucleotide sequences) uses as defaults a word length (W) of 11, alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands. The BLASTP program (for amino acid sequences) uses as defaults a word length (W) of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

Please replace the paragraph beginning at page 77, line 17, with the following rewritten paragraph:

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among B cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation in, for example, tolerant versus immunosuppressed cells, rested, naïve or activated cells, or in a healthy B cell response versus an abnormal B cell response. Genes can be turned on or turned off in a particular state, relative to another state. Any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which can be detectable by standard techniques in one such state or cell type, but can be not detectable in both. Alternatively, the determination can be quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify using standard

characterization techniques, for example, by using Affymetrix ~~GeneChip~~ GENECHIP™ expression arrays (Lockhart, *Nature Biotechnology*, (1996) 14:1675-1680; this reference and all references cited therein are incorporated by reference). Other methods include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. Preferably the change or modulation in expression (*i.e.*, upregulation or downregulation) is at least about 5%, more preferably at least about 10%, more preferably, at least about 20%, more preferably, at least about 30%, or more preferably by at least about 50%, or at least about 75%, and more preferably at least about 90%.

Please replace the paragraph beginning at page 79, line 18, with the following rewritten paragraph:

FK506, a commonly used immunosuppressant drug, can block B cell activation and can be a phenocopy of tolerance. B cells were stimulated as for FIG. 1 but in the presence of 10 ng/ml FK506. This concentration was chosen as it is within the range maintained in the blood of kidney and liver transplant patients receiving FK506 (also called Tacrolimus and Prograf~~; information on dosing from http://www.fujisawa.com/info/medinfo/mnpginst.htm~~). Of the 59 genes defined previously as increasing or decreasing 1 hr after B lymphocyte activation, only one third of these were efficiently suppressed by this dose of FK506 (FIG. 3). Some early response genes (for example, gadd153) were superinduced in the presence of drug. By this analysis, the suppressive effects of FK506 on lymphocyte activation are much more limited than the suppression achieved by peripheral tolerance. The response genes blocked by the drug include genes that are triggered by self-antigen, such as Egr-2 and CD72, which can contribute to the active maintenance of tolerance. Cells stimulated in the presence of FK506 do not activate NFAT, NFkB nor JNK though signaling through Erk is intact. Self-antigen causes apparent activation of more signaling pathways, as signaling through both Erk and NFAT is intact, but the response to antigen measured by transcript profiling is much more repressed than is achieved by FK506.